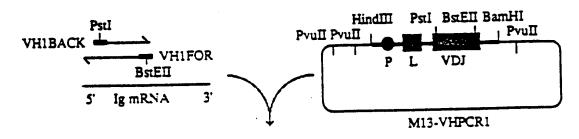


FIG. 1



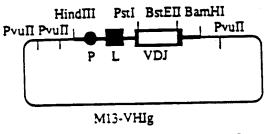
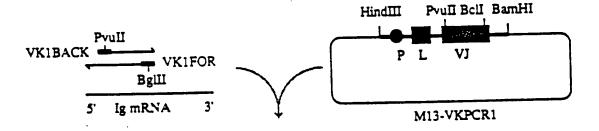


FIG. 2



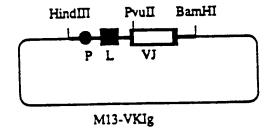


FIG. 4



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Sequence of MBrl VK

α-Lys 30

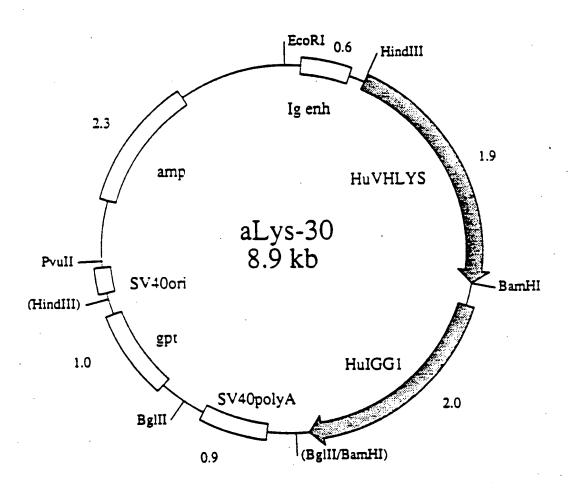
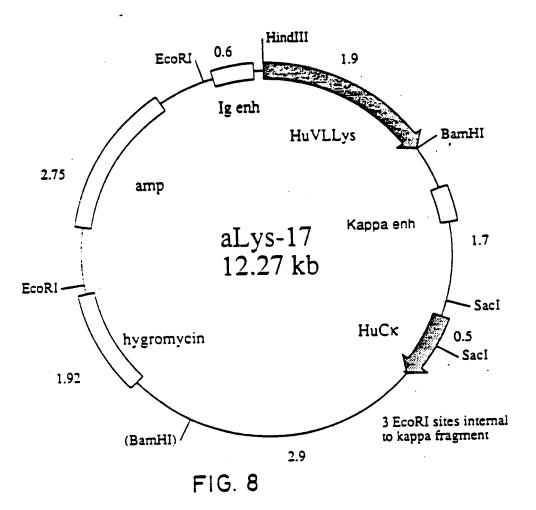
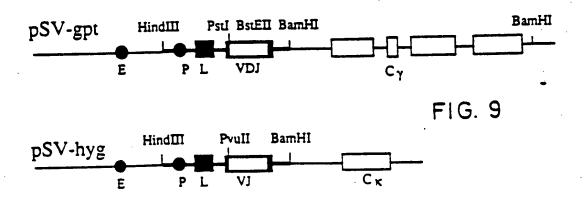


FIG. 7





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KA	BAT IB	, m. e. · ·	w.mgppokgliwl3	WIWAGGITNYNSALMS
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K.	ABAT IIA			
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K	ABAT IIB			
)	AELYYFGASYYMSIYASGYTFT AELYYFGASYMLSIKASGYTFT	24M11 24M11 24M11 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16 24M16	WANGSEGGOTENTS WANGSEGGOTENTS	EIDPSDSYTHYNGKFKG DIYPGSGSTTNYNEKFKS RIDPNSGGTKYNEKFKS EINPSNGGTNYNEKFKS DIYPGSGSTNYNEKFKS DIYPGSGSTNYNEKFKS AIDPETGGTAYNOKFKG WIYPGSGGTNYNEKFKG WIYPGSGTNYNOKFKG WIYPGSGTNYNOKFKG NIDPSDSETHYNGKFKG NIDPSDSETHYNGKFKG NIDPSDSETHYNGKFKD DIYPGSGSTNYNEKFKS SFTMYSDATEYSENFKG DIYPGSGSTNYNEKFKS
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i	ABAT III B			
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FIG. 10 a

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KATIT/TTSSSTAYMCLSSLTSEDSA/TYCAR
KATITITIKSSSTAYKQLSSLTSEDSANYYCA:
KATLT/EXSSST/YLELSRLTSDDSX/YYCAF
KATLT/DXSSSTAYMQLSSLTSEDSA/YYCA/
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PS.gene
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Unproductive

RFTISRONAWITLFLOYTSLRSEDTAMYYCAR RFTISRONTWMTLYLOMSSLRSEDTALYYCAR RFTISRONSWITLYLOMISLRAEDTAVYYCAI RFTISRONSWITLYLOMISLRAEDTAVYYCAI	;
RFIISRONSKUTLYLOMSSLRSEDTALYYGA RFIISRONSKUTLYLOMSSLRAEDTAVYYGA RFIISRONTKUTLYLOMSSLRSEDTALYYGA RFTISRONAKUTLYLOMSSLKSEDTALYYGA	7

AKFHLYFDY REGYVESRLOGOV RGLHWFDF RNYGSSPFDY PPHERBY 43 nt. 28 nt. 35 nt.

Ps.gene Ps.gene Ps.gene Ps.gene/Unproductiv Ps.gene/Unproductiv Unproductive

RETISRODSKSRVYLOWNSLRAEDTHIYYOTG

3C == 1.

Unproductive

KATLTACKSSST/KYELSPLTSSCSA/YFCAP

HEDROSSGYAYO:

FIG. 10 b

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10/23

CDR_2	FRANKHORY 3	CDR_3
KABAT BUMAN VEL		
GYAQKFQG	STSTAYMELRSLRSEDTAVVYCAR RVTTRRHKSTSTAYMELSSLRSEDTAVYYCAR RVTMTRATSISTATMELSSLRSEDTAVYYCAR	GEGWDHEDY GSRYGYDCSGYYYL LAHFSGSPVDWFDF
KS	RVTISVDTSKIKÇFSLKLSSVTAADTAVYYCAR RVTISVDTSKIKÇFSLKLSSVTAADTAVYYCAR RLSISQDTSRIKÇFSLRLSSVTAADTAVYYCAR ESTSTAYMELSSLRSEDTAVYYCAR	GGVVPAAIMDV MARYYDFWSGYSAYYDY HRNWGSPVHFDY DSYGDYGGHY
KABAT BUMAN VES		
ISYITSSSSYTNYADSVKG SVKG YADSVKG YADSVKG PSVKG DSVKG VSAISGSGSTYYADSVKG AVISYDGSNKYYADSVKG GAVISYDGSNKYYADSVKG	RETISRDNAKNSLYLCMNSLRADDTAVYYCAR RETISRDDSKSIAYLCVNSLKTEDTAVYYCTR RETISRDNAKNSLFLCMSSLRAEDTAFYYCAR RETISRDNSKNTLYLCMNSLRAEDTAVYYCAR RETISRDNAKNSLYLCMNSLRDEDTAVYYCAR RETISRDNFKNTLYLCMNSLRSEDTAVYYCAR RETISRDNSKNTLYLCMNSLRAEDTAVYYCAR RETISRDNSKNTLYLCMNSLRAEDTAVYYCAR AKNSLYLCMNSLRAEDTAVYYCVR RETISRDDSKNSLYLCMNSLNTEDTAVYYCVR	DGREGTYSPSDY TIYYDSSGYPYW GIALDAFDI S3 NT. UNPROD REARR DHSGTGGGGSGSYF KDNLWFDP DLGGRGVVVVPAPGGRSIYYYGMDV LEGIGTIYYYGMDV DDSSSWPKHFQH SGVVPYLDY
KNOWN FAMILY		
		DPRIAARPDYYYYMDV GAEVVEFTARYYYGLNV

## <u>*</u>	TE:	FR2
Y	SYGIS	WYTTGPWTROLRWMG
GEKPGSSVKVSCKASGYTFT	DAŁW.	WMRCAPGCRLEWMG
QVQLQEIGPRIGEASETLSLICAVSGDSIS	SGNW-I	wvroppgkglewig
QVQLQESG?GLVK*SETLSLTCTVSGGSIS	SYYWS	MIzobbCKCTEMIC
CALL:	MAGWE	WVRQDHAQGLEWMG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS	SGNW":	WVRCPPGKGLEWIG
GPRIGEASETISTICTVSGGSIS	SSSYYw	Wiroppokglewig
QVQLQESGPGLVKpSETLSLTCTVSGGSIS	Syyws	Wiroppgkglewig
LSLICAVSGSSIS	SGNW" I	wvroppgkglewig
SETISLTCAVYGGSFS	GXXM2	wiroppokalewia
CVCT/CSCYEAKCGYZAZAKAZCKYZCKYZZALET	MACATE	WVRCVLAQGLEWMG
SETLSLICAVSGDSIS	SGNW" I	WVRQPPGKGLEWIG
SRACTGEASETLSLTCTVSGGSIS	SSSYYWG	WIROPPGKGLEWIG
CPLICTVSGGSVSSGS	YYWS	WIROPPGKGLEWIG
GLVKØSETLSLTCTVSGGSIS	SYYWS	WIGSPPGKGLEWIG
STETLSLICAVSGDSIS	SGNW-I	WVRQPPGKGLEWIG
GYGLYGSGAEVKKRGSSYKYSCKASGGTFS	SYAIS	WVRCAPGOGLEWMG
CVCLCCWGAGLLICE SETLSLTCAVY GGSFS	GYYWS	WIRCPPGKGLEWIG
QUQUESGPOLVKPSETLSLTCT/SGGSIS	SSSYYWG	WIRCPPCKGLEWIG
GPGLYRCE SQTLSLTCTVSGGSLS	SGGYYNS	MIRCNECKCIEMIC

• indicates stop todon (unsure as sequence remains in frame)
• sequence termonates due to internal restriction site

lower case denotes frame shift

	253					
ST SAYNGITTI YACKLOG	RVIMITOISISIAYMELRELREDDIAVYYCAR	DIVS				
MINGNG:TXYSQKLQG	RVTITRDTSASTAYMQLSSLRSEDTAVYYCAR	DIVS				
EIHHEGETYYNDETKE	RITYSVOTSKNCFYLKLSS.					
RIYISGSTNYNPSLKS	RVTISVDTSKNGFSLKLSSVTAADTAVYYCAR	DIVS				
LVCPSEGSTSYAQKFQA	RVTITRDTSMSTAYMELSSLRSEDTAMMYCAR	DIVS				
EIHHSGSTYYNPSLKS	RITMSVDTSKNCFYLKLSS.					
EINHSGSTNYNPSLKS	RVIISVDISKNCFSLKLSS.					
YIYYSGSTNYNZSLKS	RVTISVDTSKNQFSLKLSS.					
EIHHSGSTYYNPSLKS	RITMSVDTSKNOFYLKLSS.					
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DIV				
	RVTITRDTSMSTAYMELSSLRSEDTAMYYCAR	DIV				
LVCPSDGSTSYAQKFQA EIHHSGSTYYNPSLKS	RITMSVDTSKNOFYLKLSS.					
SIYYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLSS•					
AIAAECSINANASTK2	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DIV				
	RVTM5VDTSKNQF5LKLSS•					
RIYTSGSTNYNPSLKS	RITMSVDTSKNGFYLKLSS.					
EIHHSGSTYYNPSLKS	RVTITADKSTSTAYMELSSLRSEDTAVYYCAR	DTV				
RIIPILGIANYAQKEQG	RVIISVDISKNÇFSLKLSS.					
EINHSGSTNYNPSLKS	RVIISVDISKNÇFSLKLSS•					
AINASCELANUASTKE	RVTISVDTSKNCFSLKCSSVTAADTAVYYCAR	DTV				

FIG. 12

12/23

pSW_

HindIII site AAGCTT

M K Y L L P T A A

GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A 3 L L L L A A Q P A M A Q V Q L Q E S GCTSGATTSTTATTACTCSCTSCCCAACCAGCGATGCCAGGTGCAGGTGCAGGAGTCA 120

G F G L V A F S C S L S I T C T V S G F GGACCTGGCGTGTGGGGGGGTTCAGAGGGTTC 130 140 150 160 170 . 180

S L T G Y G V N W V R Q P P G K G L E W TGATTAACGGGTATGGTGTAACTGGGTTGGCCAGCGTCCAGGAAAGGGTCTGGAGTGG 190 200 210 220 230 240

L G M I W G D G H T D Y N S A L K S R L CTGGGAATGATTTGGGGTGATGGAACAGACTATAATTCAGCTCTCAAATCCAGACTG 250 260 290 300

S I S K D N S K S Q V F L K M N S L H T AGCATCAGCAAGTCTGCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC 370 380 390 400 410 420

Q G T T V T V S S SMAI

CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCGGGGCTAAGCTCGAATTC

430 440 450 460 470 480

HindIII AAGCTT

M K Y L L P T A A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A C P A M A Q V Q L Q E S GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGCCAGGTGCAGGTGCAGGAGTCA 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F GGACCTGGCCTGGGGGGCCCTCACAGAGCCTGTCACATGCACGGCTCTCAGGGTTC 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W TCATTAACCGGCTATGGTGTAAACTGGGTTCGGCAGCCTCCAGGAAAGGGTCTGGAGTGG 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG 250 250 250 200 300

S I S K D N S K S Q V F L K M N S L H T AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G GATGACACAGCTACTGTGTGTGTGTAGAGAGAGATTATAGGCTTGACTACTGGGGC 370 380 390 400 410 420

Q G T T V T V S S CAASGCACGCCAAGCTTGCATGC 430 440 450 460 470 480

M K Y L L P T A A A G

AAATTOTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA
490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCCCAACCAGCGATGGCCGACATCGTCCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT 610 620 630 640 650 660

H N Y L A W Y 2 Q K Q G K S P Q L L V Y CACAATTATTTAGCATGGTATCAGCAGAAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT 670 680 690 700 710 720

FIG. 14 a

Y T T T L A D G V P S R F S G S G S G T TATACAACAACCTTAGCAGTGGTGGTGGCAGTGGAACA 730 740 750 760 770 780

Q Y S L K I N S L Q F E D F G S Y Y C Q CANTATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTITIGGAGTACTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC 910

FIG. 14 b

pSWIHPCLYMYC .

HindIII site AAGCTT

M K Y L L P T A A

GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC

10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGCCCAGGTGCAGCTGCAG

Polylinker TCTAGA GTCGAC CTCGAG XbaI SalI XhoI

MYC PEPTIDE

V T V S S <u>F O K L I S F E D L N</u>

GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGGATCTGAATTAATAA

BStEII

GGGCTAAGCTCGAATTC

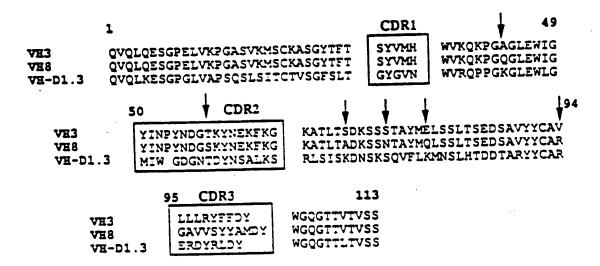
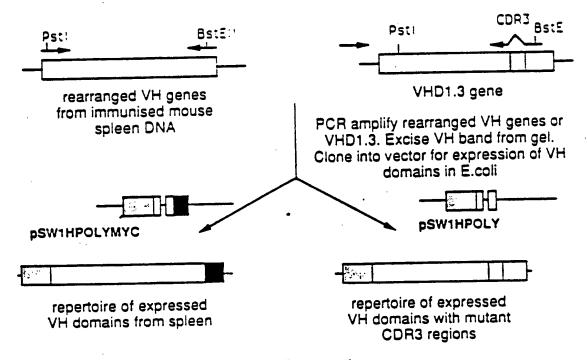


FIG. 16

FR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS	
	SYAMS	CDR1
FR2	WVRQAPGKGLEWVS	
	AISGSGGSTYYADSVKG	CDR2
FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAM	1
	WRGIATPVSFDLGYFDY	CDR3

FIG. 17



Assay for binding to antigen

FIG. 18

pSW2HPCLY

HindIII AAGCTT

MKYLLPIAA GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAAATACCTATTGCCTACGGCAGCC 40 50 20 30 10

A G L L L A A Q P A M A Q V Q L Q GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGCAGCTGCAGCTGCAG 70 80 9C 100 110 PStI

TCTAGA GTCGAC CTCGAG XbaI SalI XhoI

V T V S S
GGTCACCSTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC BSTEII 43C 44C 450 460 470 480

MKYLLPTAAAG AAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA 490 500 510 520 530 540

L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCCGACCAGCGACAGCGACACCGTCCTGACTCAGCCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I TOCOTTTOTS CSTOTS TOS CAGANACTS TOACCATOACATGTC CAGCAAGTGGGAATATT 610 620 650 660

H N Y L A W Y Q Q K Q G K S F Q L L V Y CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT 670 680 690 700 710 720 680 690 700 710 720

Y T T L A D G V P S R F S G S G S G T TATACAACAACOTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA 73C 740 75C 760 770

Q'Y S L K I N S L Q P E D F G S Y Y C Q CĂĂTĂTTCTCTCĂĂGĂTCĂĂCĂĞCCTGCĂĂCCTGĂĀGĂTTTTGĞGĀĞTTĂTTĀCTĞTCĀĀ 790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R CATTITTGGAGTACTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA 850 860 870 880 890

TAAGAGCTCGAATTC 910

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						· ·							K					
AG(::T	3CAT 10	SCAA	ATTC	20			3C		370	40		.	AC.	50 50		JUTA	60 60
A	A	A	G L	L	L	L	A	A	Q	P	A	M	A	Q	V	Q	L	Q
CA:	GCC	50TG 70		G2	8C		3 C 1 .	90		سنحار	100))	3000		10		- 1 (5)	120
E	S	G	P G	L	v	A	P	S	Q	S	L	S	I	I	C	; ;	V	S
MG	I'CA	3AC 130			14C	ucu,		150		AGC:	160)	٠. ٠	1	70	MCC.	310	180
G	Ī	S TCAT	L I	G	<u> </u>	G	V	N	W	<u>v</u>	R	Q	P	P	G	K	G	L
, , , , , , , , , , , , , , , , , , ,		190			200	3 61,	3170	210		9.11	220		· · · ·	2	30	nnu	-	240
E	W	i Ciga	G N	4 I	*	G	D	G	N 227	I 2024	D 72.01	Y	N 22T	S	A	L	K	S
an J	. 30	250	ion.	. JA.	260	JG _ \	3 0.2	270		nun.	29	C	-	2	90			300
R	L	S AJCA	I	s K		N	S	K 110	s	Q	V.	F	L	K AAA	M ATG	N AAC	S AGT	L
130		310						33C			34	Ċ		3	50			360
# -1-1-1	<u>.</u>	: :3\:13	3 3	. A	. R 0200	Y Sac	Y Tac	C TST	A GCC	R 'AGA	E GAG	R AGA	ت جمع	Y TAI	R 'XGG	L	GAC	Y
~~~		370	;		380			390			40	0		4	10			420
<b>*</b>	S	0 ::::::::::::::::::::::::::::::::::::	G :	: : ::::::::::::::::::::::::::::::::::	V SGT	: ממגי	V STC	S TCC	S TCA	G .GGT	G GGT	G GGT	A GCT	P CCA	A GCA	A GCT	A SC2	P
		430			440			450			46	٥		4	70			480
A	G	S NGSAC	G (	g v Last	, G	L	K AAG	E GAG	s TC2	G GGA	P	G GGC	L CTG	V GTG	A GCC	P CCC	S TC	Q ACAG
		490			500			510			52	0		5	30			540
S AG:	_	S STCC	: ATCA	T C	. T	V ESTO	S TC	G NGGG	F	S ETCA	L STA	T ACC	G :GGC	Y TA:	G :GG:	V STD:	N SAAS	W CTGG
		550	0		560			570			58	0		5	9C			600
٧ <del>[]</del>	R Togo	Q :::>G(	P CCTC	ም	K AAA	G BGGI	CIC	E.	· W	L SCTG	G GGA	M Ato	I ATT	W TIG	G GG:	D CGA:	e Ceer	N AAAC
		61	С		620			630	;		64	C		•	550			660
T AC	D AGA	Y CTAT	n Aatt	S A	L	K Caaa	S	R CAGA	L	S Sago	I ATC	S LAGO	K Caac	D SGA	n Caac	S STC	K Caa	S GAGC
		67	0		68C			690	)		70	00		•	710			720
Q CA	V AGT	F IIIC	L TTAA	K N	1 N TGAA	S CAG:	L	H SCAC	T CAC	D IGA:	D GAC	T L)(L)	A AGC	R Cago	Y GTA	Y CTA:	CIG C	A TGCC
		73	0		740			750	)		76	50		•	770			780
R AG	E Aga	r Gaga	D GATI	Y I	R L SGCT	D TGAC	Y AT:	w CTGC	و اوود	و بلات	G AGG(	T CAC	T CAC	V GGT	T CAC	V CGT	S CTC	S CTCA
•	•	79	_		800			810				20			830			840
TA	λτλ	agag 85																

FIG. 20

BUDSTITUTE OHERT

- G P G L V A P S Q S L S I T C T V S G F GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC 130 140 150 160 170 180
- S L T G Y G V N W V R Q P P G K G L E W TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG 190 200 210 220 230 240
- L G M I W G D G N T D Y N S A L K S R L CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG 250 260 270 280 290 300
- S I S K D N S K S Q V F L K M N S L H T AGCATCAGCAAGGACAACTCCAAGAGTCTTCTTAAAAATGAACAGTCTGCACACT 310 320 330 340 350 360
- D D T A R Y Y C A R E R D Y R L D Y W G GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC 370 380 390 400 410 420
- Q G T T V T V S S R T P E M P V L E N R CAAGGCACCACGGTCACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG 430 440 450 460 470 480
- A A Q G D I T A P G G A R R L T G D Q T GCTGCTCAGGGGGATATTACTGCACCGGGGGGTGCTCGCCGTTTAACGGGTGATCAGACT 490 500 510 520 530 540
- A A L R D S L S D K P A K N I I L L I G GCCGCTCTGCGTGATTCTCTTAGCGATAAACCTGCAAAAAATATTATTTTGCTGATTGGC 550 560 590 600

- K K T G K P D Y V T D S A A S A T A W S AAAAAAACCGGCAAACCGGACTACGTCACCGACTCGGCTGCATCAGCAACCGCCTGGTCA 730 742 750 760 760 770 780

FIG. 21 a

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- TOWKTYNGALGVDIEKDHP

  TOWKTYNGALGVDIEKDHP

  ACCGGTGTCAAAACCTATAACGGCGCGCTGGGCGTCGATATTCACGAAAAAGATCACCCA

  ACCGGTGTCAAAACCTATAACGGCGCGCTGGGCGTCGATATTCACGAAAAAGATCACCCA

  840

  840
  - T I L E M A K A A G L A T G N V S T A E ACGATTCTGGAAATGGCAAAAGCCGCAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG 850 850 890 900
  - L Q D A T P A A L V A H V T S R K C Y G
    TTGCAGGATGCCACGCCGCTGCTGGTGGCACATGTGACCTCGCGCAAATGCTACGGT
    910 920 930 940 950 960
  - P S A T S E K C P G N A L E K G G K G S CCGAGCGCGACCAGTGAAAAATGTCCGGGTAACGCTCTGGAAAAAGGCGGAAAAGGATCG 970 980 990 1000 1010 1020

  - F A E T A T A G D W Q G K T L R E Q A Q TTTGCTGAAACGCAACAGGCACAG 1090 1100 1110 1120 1130 1140
  - A R G Y Q L V S D A A S L N S V T E A N GEGEGTGGTTATEAGTTGGTGAGEGAATGCTGACTGAATTCGGTGACGGAAGCGAAT 1150 1160 1170 1180 1190 1200
  - C Q K P L L G L F A D G N M P V R W L G CAGCAAAAACCCCTGCTTGGCCTGTTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA 1210 1220 1230 1240 1250 1260
  - P K A T Y H G N I D K P A V T C T P N P CCGAAAGCAACGTACCATGGCAATTCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG 1270 1280 1290 1300 1310 1320
  - Q R N D S V P T L A Q M T D K A I E L L CAACGTAATGACAGTGTACCAACCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG 1330 1340 1350 1360 1370 1380
    - S K N E K G F F L Q V E G A S I D K Q D AGTAAAAATGAGAAAGGCTTTTTCCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT 1390 1400 1410 1420 1430 1440
    - H A A N P C G Q I G E T V D L D E A V Q CATGCTGCGAATCCTTGTGGGCAAATTGGCGAGACGGTCGATCTCGATGAAGCCGTACAA 1450 1460 1470 1480 1490 1500
    - RALEFAKKEGNTLVIVTADH
      CGGGCGCTGGATCGCTGATCACCGCTGGATCAC
      1510 1520 1530 1540 1550 1560

FIG. 21 b

A H A S Q I V A P D T K A P G L T Q A L GCCCACGCCAGACAGATTGTTGCGCCGGATACCAAAGCTCCGGGCCTCACCCAGGCGCTA 1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q AATACCAAAGATGGCGCAGTGATGGTGATGAGTTACGGGAACTCCGAAGAGGATTCACAA 1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V GAACATACCGGCAGTCAGTTGCGTATTGCGGCGTATGGCCCGCATGCCGCCAATGTTGTT 1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGACCAGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGGAGTGAATTTTCGCTGCCGGGTGGTTTTTTTGCTGTTAGC 1810 1820 1830 1840 1850

FIG. 21c

- M K Y L L P T A A GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC 10 20 30 40 50 60
- A G L L L L A A Q P A M A Q V Q L Q E S GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA 70 80 90 100 110 120
- G P G L V A P S Q S L S I T C T V S G F GGACCTGGCCTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC 130 140 150 160 170 180
- S L T G Y G V N W V R Q P P G K G L E W TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG 190 200 210 220 230 240
- L G M I W G D G N T D Y N S A L K S R L CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG 250 260 270 280 290 300
- S I S K D N S K S Q V F L K M N S L H T AGCATCAGGAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT 310 320 330 340 350 360
- D D T A R Y Y C A R E R D Y R L D Y W G GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC 370 380 390 400 410 420

  - M K Y L L P T A A A G L
    TTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
    490 500 510 520 530 540
  - L L L A A Q P A M A D I E L V D L E I K
    TTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
    550 560 570 580 590 600
  - R E Q K L I S E E D L N * *
    CGGGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
    £10 620 630 640 650 660

GATCCAGCTCGAATTC 670

Q V Q L Q E S G P G L V Q P S Q S L S I 30 10 20 40 50 T C T V S G F S L T S Y G V H W V R Q S 70 120 80 90 100 110 PGKGLEWLGMIWGDGNTDYN 130 140 150 160 170 SALKSRLSISKDNSKSQV.FL TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTA 190 200 210 220 230 K M N S L H T D D T A R Y Y C A R E R D 

FIG. 23

320 330 340

Y R L D Y W G Q G T T V T V S S TATAGGGTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

31C